

GenInfo version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: March 14, 2002, 17:34:11 ; Search time 91.4 seconds
(without alignments)
20,827 Million cell updates/sec

Title: US-09-786-009-7
Perfect score: 69
Sequence: 1 MAMG381P0550.14

Scoring table:
Gap: 10.0 ; Gapext: 0.5

Searched: 473505 seqs, 14627229 residues

Total number of hits satisfying chosen parameters: 473505

Minimum DB seq length: 0
Maximum DB seq length: 208030000

Post-processing: Minimum Match: 0.8
Maximum Match: 100%

Listed first 45 summaries

Database:

1: SP archaea:***
2: SP bacteria:***
3: SP fungi:***
4: SP human:***
5: SP invertebrate:***
6: SP mammal:***
7: SP insect:***
8: SP ornithine:***
9: SP plant:***
10: SP fungi:***
11: SF toad:***
12: SF virus:***
13: SF vertebrate:***
14: SF invertebrate:***

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match Length	DB ID	Description
1	43	62.3	722 2	090808
2	42	60.9	1386 4	090808
3	41	59.4	234 2	053715
4	41	59.4	430 5	090584
5	41	59.4	430 5	090584
6	41	59.4	541 10	082416
7	41	59.4	542 5	090422
8	41	59.4	578 5	017444
9	40	58.2	430 10	080428
10	40	58.2	719 10	064794
11	40	58.2	1405 5	090408
12	39	57.5	1701 10	082622
13	38	55.1	186 2	087657
14	38	55.1	298 2	091351
15	38	55.1	435 10	090980
16	38	55.1	445 10	091098
17	38	55.1	476 4	012618
18	38	55.1	476 4	012618
19	38	55.1	608 10	082414

20	38	55.1	512 1	082414
21	38	55.1	518 1	082414
22	38	55.1	525 1	082414
23	38	55.1	552 1	082414
24	38	55.1	1074 4	080505
25	38	55.1	1147 4	080505
26	38	55.1	1407 1	080505
27	38	55.1	1407 1	080505
28	38	55.1	1407 1	080505
29	37	54.6	1407 1	080505
30	37	54.6	1407 1	080505
31	37	54.6	1407 1	080505
32	37	54.6	1407 1	080505
33	37	54.6	1407 1	080505
34	37	54.6	1407 1	080505
35	37	54.6	1407 1	080505
36	37	54.6	1407 1	080505
37	37	54.6	1407 1	080505
38	37	54.6	1407 1	080505
39	37	54.6	1407 1	080505
40	37	54.6	1407 1	080505
41	37	54.6	1407 1	080505
42	37	54.6	1407 1	080505
43	37	54.6	1407 1	080505
44	37	54.6	1407 1	080505
45	37	54.6	1407 1	080505

ALL MEN

Result 1

ID 090808

AC 090808

DT 01-MAY-2000

DT 01-JUN-2001

DE HYPOHETICAL 77.3 KDA PROTEIN.

WE 77.3

OS Acinetobacter lwoffi.

OC Bacterium Proteobacteria

CC Acinetobacter

CC NCBI TaxID: 28094

FN 111

KE SUGGESTED FROM N.A.

KE STRAIN KAS-1

KA Nakai, D., Gutnick, D.L.

KT required for emulsan biosynthesis

KL Submitted (JUN 1999) to the EMBL/GenBank/

FN 121

KE SUGGESTED FROM N.A.

KE STRAIN KAS-1

KA Nakai, D., Gutnick, D.L.

KT required for emulsan biosynthesis

KL Submitted (JUN 1999) to the EMBL/GenBank/

FN 121

KE SUGGESTED FROM N.A.

KE STRAIN KAS-1

KA Nakai, D., Gutnick, D.L.

KT required for emulsan biosynthesis

KL Submitted (JUN 1999) to the EMBL/GenBank/

FN 121

KE SUGGESTED FROM N.A.

KE STRAIN KAS-1

KA Nakai, D., Gutnick, D.L.

KT required for emulsan biosynthesis

KL Submitted (JUN 1999) to the EMBL/GenBank/

FN 121

KE SUGGESTED FROM N.A.

KE STRAIN KAS-1

KA Nakai, D., Gutnick, D.L.

KT required for emulsan biosynthesis

KL Submitted (JUN 1999) to the EMBL/GenBank/

FN 121

KE SUGGESTED FROM N.A.

KE STRAIN KAS-1

KA Nakai, D., Gutnick, D.L.

KT required for emulsan biosynthesis

KL Submitted (JUN 1999) to the EMBL/GenBank/

FN 121

KE SUGGESTED FROM N.A.

KE STRAIN KAS-1

KA Nakai, D., Gutnick, D.L.

KT required for emulsan biosynthesis

KL Submitted (JUN 1999) to the EMBL/GenBank/

FN 121

KE SUGGESTED FROM N.A.

KE STRAIN KAS-1

KA Nakai, D., Gutnick, D.L.

KT required for emulsan biosynthesis

KL Submitted (JUN 1999) to the EMBL/GenBank/

FN 121

KE SUGGESTED FROM N.A.

KE STRAIN KAS-1

KA Nakai, D., Gutnick, D.L.

KT required for emulsan biosynthesis

KL Submitted (JUN 1999) to the EMBL/GenBank/

FN 121

KE SUGGESTED FROM N.A.

KE STRAIN KAS-1

KA Nakai, D., Gutnick, D.L.

KT required for emulsan biosynthesis

KL Submitted (JUN 1999) to the EMBL/GenBank/

FN 121

KE SUGGESTED FROM N.A.

KE STRAIN KAS-1

KA Nakai, D., Gutnick, D.L.

KT required for emulsan biosynthesis

KL Submitted (JUN 1999) to the EMBL/GenBank/

FN 121

KE SUGGESTED FROM N.A.

KE STRAIN KAS-1

KA Nakai, D., Gutnick, D.L.

KT required for emulsan biosynthesis

KL Submitted (JUN 1999) to the EMBL/GenBank/

FN 121

KE SUGGESTED FROM N.A.

KE STRAIN KAS-1

KA Nakai, D., Gutnick, D.L.

KT required for emulsan biosynthesis

KL Submitted (JUN 1999) to the EMBL/GenBank/

FN 121

KE SUGGESTED FROM N.A.

KE STRAIN KAS-1

KA Nakai, D., Gutnick, D.L.

KT required for emulsan biosynthesis

KL Submitted (JUN 1999) to the EMBL/GenBank/

FN 121

KE SUGGESTED FROM N.A.

KE STRAIN KAS-1

KA Nakai, D., Gutnick, D.L.

KT required for emulsan biosynthesis

KL Submitted (JUN 1999) to the EMBL/GenBank/

FN 121

KE SUGGESTED FROM N.A.

KE STRAIN KAS-1

KA Nakai, D., Gutnick, D.L.

KT required for emulsan biosynthesis

KL Submitted (JUN 1999) to the EMBL/GenBank/

FN 121

KE SUGGESTED FROM N.A.

KE STRAIN KAS-1

KA Nakai, D., Gutnick, D.L.

KT required for emulsan biosynthesis

KL Submitted (JUN 1999) to the EMBL/GenBank/

FN 121

KE SUGGESTED FROM N.A.

KE STRAIN KAS-1

KA Nakai, D., Gutnick, D.L.

KT required for emulsan biosynthesis

KL Submitted (JUN 1999) to the EMBL/GenBank/

FN 121

KE SUGGESTED FROM N.A.

KE STRAIN KAS-1

KA Nakai, D., Gutnick, D.L.

KT required for emulsan biosynthesis

KL Submitted (JUN 1999) to the EMBL/GenBank/

FN 121

KE SUGGESTED FROM N.A.

KE STRAIN KAS-1

KA Nakai, D., Gutnick, D.L.

KT required for emulsan biosynthesis

KL Submitted (JUN 1999) to the EMBL/GenBank/

FN 121

KE SUGGESTED FROM N.A.

KE STRAIN KAS-1

KA Nakai, D., Gutnick, D.L.

KT required for emulsan biosynthesis

KL Submitted (JUN 1999) to the EMBL/GenBank/

FN 121

KE SUGGESTED FROM N.A.

KE STRAIN KAS-1

KA Nakai, D., Gutnick, D.L.

KT required for emulsan biosynthesis

KL Submitted (JUN 1999) to the EMBL/GenBank/

FN 121

KE SUGGESTED FROM N.A.

KE STRAIN KAS-1

KA Nakai, D., Gutnick, D.L.

KT required for emulsan biosynthesis

KL Submitted (JUN 1999) to the EMBL/GenBank/

FN 121

KE SUGGESTED FROM N.A.

KE STRAIN KAS-1

KA Nakai, D., Gutnick, D.L.

KT required for emulsan biosynthesis

KL Submitted (JUN 1999) to the EMBL/GenBank/

FN 121

KE SUGGESTED FROM N.A.

KE STRAIN KAS-1

KA Nakai, D., Gutnick, D.L.

KT required for emulsan biosynthesis

KL Submitted (JUN 1999) to the EMBL/GenBank/

FN 121

KE SUGGESTED FROM N.A.

KE STRAIN KAS-1

KA Nakai, D., Gutnick, D.L.

KT required for emulsan biosynthesis

KL Submitted (JUN 1999) to the EMBL/GenBank/

FN 121

KE SUGGESTED FROM N.A.

KE STRAIN KAS-1

KA Nakai, D., Gutnick, D.L.

KT required for emulsan biosynthesis

KL Submitted (JUN 1999) to the EMBL/GenBank/

FN 121

KE SUGGESTED FROM N.A.

KE STRAIN KAS-1

KA Nakai, D., Gutnick, D.L.

KT required for emulsan biosynthesis

KL Submitted (JUN 1999) to the EMBL/GenBank/

FN 121

KE SUGGESTED FROM N.A.

KE STRAIN KAS-1

KA Nakai, D., Gutnick, D.L.

KT required for emulsan biosynthesis

KL Submitted (JUN 1999) to the EMBL/GenBank/

FN 121

KE SUGGESTED FROM N.A.

KE STRAIN KAS-1

KA Nakai, D., Gutnick, D.L.

KT required for emulsan biosynthesis

KL Submitted (JUN 1999) to the EMBL/GenBank/

FN 121

KE SUGGESTED FROM N.A.

KE STRAIN KAS-1

KA Nakai, D., Gutnick, D.L.

KT required for emulsan biosynthesis

KL Submitted (JUN 1999) to the EMBL/GenBank/

FN 121

KE SUGGESTED FROM N.A.

KE STRAIN KAS-1

KA Nakai, D., Gutnick, D.L.

KT required for emulsan biosynthesis

[illegible][illegible]

DB 409 G3CRH3SCG 40%

RESULT 5

Q9N927 PRELIM NAME: PRT: 499 AA.

Q9N927:

01-OCT-2000 (TREMUR: 15, last sequence update)

01-OCT-2000 (TREMUR: 15, last sequence update)

01-JUN-2001 (TREMUR: 17, last annotation update)

01-JUN-2001 (TREMUR: 17, last annotation update)

Q9N927:

Q9N927:

Q9N927:

Q9N927:

Q9N927:

Q9N927:

Q9N927:

Q9N927:

Q9N927:

Q9N927:

Q9N927:

Q9N927:

Q9N927:

Q9N927:

Q9N927:

Q9N927:

Q9N927:

Q9N927:

Q9N927:

Q9N927:

Q9N927:

Q9N927:

Q9N927:

Q9N927:

Q9N927:

Q9N927:

Q9N927:

Q9N927:

Q9N927:

Q9N927:

Q9N927:

Q9N927:

Q9N927:

Q9N927:

Q9N927:

Q9N927:

Q9N927:

Q9N927:

Q9N927:

Q9N927:

Q9N927:

Q9N927:

Q9N927:

Q9N927:

Q9N927:

Q9N927:

Q9N927:

Q9N927:

Q9N927:

Q9N927:

Q9N927:

Q9N927:

Q9N927:

Q9N927:

Q9N927:

Q9N927:

Q9N927:

Q9N927:

Query Match

Host Local Similarity 59.4%

Matches 75 Conserved 2 Mismatch 2

Q9N927:

Q9N927:

Q9N927:

Q9N927:

Q9N927:

Q9N927:

Q9N927:

Q9N927:

Q9N927:

Q9N927:

Q9N927:

Q9N927:

Q9N927:

Q9N927:

Q9N927:

Q9N927:

Q9N927:

Q9N927:

Q9N927:

Q9N927:

Q9N927:

Q9N927:

Q9N927:

Q9N927:

Q9N927:

Q9N927:

Q9N927:

Q9N927:

Q9N927:

Q9N927:

Q9N927:

Q9N927:

Q9N927:

Q9N927:

Q9N927:

Q9N927:

Q9N927:

Q9N927:

Q9N927:

Q9N927:

Q9N927:

Q9N927:

Q9N927:

Q9N927:

Q9N927:

Q9N927:

Q9N927:

Q9N927:

Q9N927:

Q9N927:

Q9N927:

Q9N927:

Q9N927:

Q9N927:

Q9N927:

Q9N927:

Q9N927:

Q9N927:

Q9N927:

Q9N927:

Q9N927:

Q9N927:

Query Match

Host Local Similarity 59.4%

Matches 75 Conserved 2 Mismatch 2

Q9N927:

Q9N927:

Q9N927:

Q9N927:

Q9N927:

Q9N927:

Q9N927:

Q9N927:

Q9N927:

Q9N927:

Q9N927:

Q9N927:

Q9N927:

Q9N927:

Q9N927:

Q9N927:

Q9N927:

Q9N927:

Q9N927:

Q9N927:

Q9N927:

Q9N927:

Q9N927:

Q9N927:

Q9N927:

Q9N927:

Q9N927:

Q9N927:

Q9N927:

Q9N927:

Q9N927:

Q9N927:

Q9N927:

Q9N927:

Q9N927:

Q9N927:

Q9N927:

Q9N927:

Q9N927:

Q9N927:

Q9N927:

Q9N927:

Q9N927:

Q9N927:

Q9N927:

Q9N927:

Q9N927:

Q9N927:

Q9N927:

Q9N927:

Q9N927:

Q9N927:

Q9N927:

Q9N927:

Q9N927:

Q9N927:

Q9N927:

Q9N927:

Q9N927:

Q9N927:

Q9N927:

Q9N927:

KA Iheolopis A.;
 KN Submitted (MAR 1999) to the EMBL/Genbank/TrEMBL databases.
 [3]
 RE SEQUENCE FROM N.A.
 RC STRAIN-CV, COLUMBIA
 KA Iheolopis A.;
 KL Submitted (MAR 1999) to the EMBL/Genbank/TrEMBL databases.
 KN [4]
 RE SEQUENCE FROM N.A.
 RC STRAIN-CV, COLUMBIA
 KA Iheolopis A.;
 KL Submitted (MAY 1999) to the EMBL/Genbank/TrEMBL databases.
 KN [5]
 RE SEQUENCE FROM N.A.
 RC STRAIN-CV, COLUMBIA
 KL X., Kaul S., Town C.D., Benito M., Treasy T.H., Haas B.,
 Kohnig C.M., Koo H., Fujii C.Y., Ulbrack T.R., Barnstead M.E.,
 Bowman C.L., White O., Niernan W.C., Fraser C.M.,
 "Arabidopsis thaliana chromosome I BAC F127 genomic sequence."
 RE Submitted (MAY 1999) to the EMBL/Genbank/TrEMBL databases.
 KN [6]
 RE SIMILARITY TO THE SPK/TKR FAMILY OF PROTEIN KINASES.
 RC EMBL: A004393; AAC18784.1; -
 RC EMBL: A011020; AAC52-00.1; -
 RC InterPro: IPR00719; Euk_Pkinase.
 RC InterPro: IPR01611; LRR.
 RC InterPro: IPR004592; LRR_out.
 RC InterPro: IPR02290; Ser_Thr_kin_act_SITE.
 RC Pfam: PF00560; LRR_5.
 RC Pfam: PF00693; Pkinase_1.
 RC SMART: SM00470; LRR_6.
 RC PROSITE: PS00011; PROTEIN_KINASE_1; 1.
 RC PROSITE: PS0108; PROTEIN_KINASE_S1; 1.
 RC Ate-binding; Kinase; Receptor; Serine/threonine-protein kinase;
 KW Transducer.
 SO SEQUENCE. 719 AA; 77171 MW; AA4EEDD24754F1 CR764;

Query Match 58.0%; Score 40; DB 10; Length 719;
 Post Local Similarity 54.5%; Prod. No. 99;
 Matches 67 Conservative 37 Mismatches 27 Indels 07 Gaps 07
 97 3 MGGDLGGSSG 1+
 111 111 11
 20 356 LGGSSVKKTKSC 96

Search Completed: March 14 2002, 17:44:16
 Run time: 657 sec

